SEQUENCE LISTING

```
<110> Sato, Taka-Aki
<120> METHOD OF PREPARING A PROTEIN ARRAY BASED ON
      BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
<130> 65823/JPW/PT
<140> Not Yet Known
<141> 2002-03-06
<160> 33
<170> PatentIn Ver. 2.1
<210> 1
<211> 4
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<220>
<221> SITE
<222> (1)
<223> Xaa=Gly, Ser, Ala or Glu
<220>
<221> SITE
<222> (4)
<223> Xaa=Phe, Ile or Leu
<400> 1
Xaa Leu Gly Xaa
  1
<210> 2
<211> 9
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
```

```
<220>
    <221> SITE
    <222> (1)
    <223> Xaa=Lys, Arg or Gln
    <220>
    <221> SITE
    <222> (2)..(5)
    <223> Xaa=any amino acid, up to 2 Xaa may be missing
    <220>
    <221> SITE
    <222> (6)
    <223> Xaa=Gly, Ser, Ala or Glu
    <220>
    <221> SITE
    <222> (9)
<223> Xaa=Phe, Ile or Leu
    <400> 2
    Xaa Xaa Xaa Xaa Xaa Leu Gly Xaa
    <210> 3
    <211> 4
    <212> PRT
    <213> Artificial Sequence
    <220>
    <223> Description of Artificial
          Sequence:source:synthesized
    <400> 3
    Ser Leu Gly Ile
      1
    <210> 4
    <211> 3
    <212> PRT
    <213> Artificial Sequence
    <220>
    <223> Description of Artificial
          Sequence:source:synthesized
```

```
<220>
<221> SITE
<222> (1)
<223> Xaa=Ser or Thr
<220>
<221> SITE
<222> (2)
<223> Xaa=any one amino acid
<220>
<221> SITE
<222> (3)
<223> Xaa=Val, Ile or Leu
<400> 4
Xaa Xaa Xaa
  1
<210> 5
<211> 15
<212> PRT
<213> human
Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
                                      10
<210> 6
<211> 15
<212> PRT
<213> rat
<400> 6
Ser Ile Ser Asn Ser Arg Asn Glu Asn Glu Gly Gln Ser Leu Glu
                                      10
                                                           15
<210> 7
<211> 15
<212> PRT
<213> mouse
<400> 7
Ser Thr Pro Asp Thr Gly Asn Glu Asn Glu Gly Gln Cys Leu Glu
```

<210> 8 <211> 4 <212> PRT

<210> 11 <211> 8 <212> PRT

<213> Artificial Sequence

```
<220>
     <223> Description of Artificial
           Sequence:source:synthesized
     <400> 8
    Glu Ser Leu Val
      1
    <210> 9
    <211> 6
    <212> PRT
<213> Artificial Sequence
    <220>
    <223> Description of Artificial Sequence:
          source:synthesized
    <400> 9
    Thr Ile Gln Ser Val Ile
     1
    <210> 10
    <211> 8
    <212> PRT
    <213> Artificial Sequence
    <220>
    <223> Description of Artificial
          Sequence:source:synthesized
    <400> 10
    Arg Gly Phe Ile Ser Ser Leu Val
                       5
```

```
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 11
Arg Glu Thr Ile Glu Ser Thr Val
                  5
<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 12
Gln Asn Phe Arg Thr Tyr Ile Val Ser Phe Val
                  5
<210> 13
<211> 13
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 13
Ser Asp Ser Asn Met Asn Met Asn Glu Leu Ser Glu Val
                                      10
<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
```

```
M
```

```
Pro Pro Thr Cys Ser Gln Ala Asn Ser Gly Arg Ile Ser Thr Leu
  1
                  5
<210> 15
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 15
Ile Asp Leu Ala Ser Glu Phe Leu Phe Leu Ser Asn Ser Phe Leu
  1
                  5
                                      10
                                                           15
<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 16
Asp Ser Glu Met Tyr Asn Phe Arg Ser Gln Leu Ala Ser Val Val
                  5
                                      10
                                                          15
<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
Ile Pro Pro Asp Ser Glu Asp Gly Asn Glu Glu Gln Ser Leu Val
                                      10
                                                          15
```

<210> 18

```
with the training of the control of
```

```
<211> 4
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 18
Gln Ser Leu Val
  1
<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:source
      synthesized
<400> 19
Ile Gln Ser Leu Val
 1
                  5
<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 20
Glu Ile Gln Ser Leu Val
<210> 21
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
```

```
Sequence:source:synthesized
<400> 21
Asn Glu Ile Gln Ser Leu Val
                   5
<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 22
Arg Asn Glu Ile Gln Ser Leu Val
  1
<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<400> 23
Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
  1
                  5
                                      10
                                                           15
<210> 24
<211> 427
<212> PRT
<213> human
<400> 24
Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
 1
                  5
                                      10
                                                           15
```

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn

Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys

25

30

20

Leu	Gly	Glu	Gly	Val	Ala	Gln	Pro	Cys	Gly	Ala	Asn	Gln	Thr	Val	Cys
	50					55					60				

- Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
 65 70 75 80
- Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser 85 90 95
- Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
 100 105 110
- Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys 115 120 125
- Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr 130 135 140
- Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His 145 150 155 160
- Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln 165 170 175
- Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro 180 185 190
- Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
 195 200 205
- Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile 210 215 220
- Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln 225 230 235 240
- Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys 245 250 255
- Ser Ile Leu Ala Ala Val Val Gly Leu Val Ala Tyr Ile Ala Phe 260 265 270
- Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gly Gly Ala Asn Ser Arg 275 280 285
- Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Ile His Ser Asp

290 295 300

Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Pro His 305 310 315 320

Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Gly Leu Tyr 325 330 335

Ser Ser Leu Pro Pro Ala Lys Arg Glu Glu Val Glu Lys Leu Leu Asn 340 345 350

Gly Ser Ala Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr 355 360 365

Gln Pro Glu His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg 370 375 380

Ala Leu Leu Ala Ser Trp Ala Thr Gln Asp Ser Ala Thr Leu Asp Ala 385 390 395 400

Leu Leu Ala Ala Leu Arg Arg Ile Gln Arg Ala Asp Leu Val Glu Ser 405 410 415

Leu Cys Ser Glu Ser Thr Ala Thr Ser Pro Val 420 425

<210> 25

<211> 458

<212> PRT

<213> human

<400> 25

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu

1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn 50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

- Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile 85 90 95
- Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu 100 105 110
- Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn 115 120 125
- Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Ile Thr Leu Glu 130 135 140
- Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
 145 150 155 160
- Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu 165 170 175
- Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys 180 185 190
- Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser 195 200 205
- Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro 210 215 220
- Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp 225 230 235 240
- Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu 245 250 255
- Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu 260 265 270
- Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu 275 280 285
- Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys 290 295 300
- Thr Gly Lys Leu His Gln Glu Asn Val Leu Val Val Met Arg Ala Thr 305 310 315 320
- Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro 325 330 335

Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser 340 350

Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp 355 360 365

Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile 370 375 380

Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile 385 390 395 400

Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile 405 410 415

Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met 420 425 430

Ser Gln Ile Lys Arg Leu Leu Ser Glu Lys Lys Glu Cys Gln Cys Pro 435 440 445

His Arg Phe Gln Lys Thr Cys Ser Pro Ile 450 455

<210> 26

<211> 828

<212> PRT

<213> human

<400> 26

Met Asn Ser Gly Val Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu

1 10 15

Leu Ser Glu Leu His Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile $20 \hspace{1cm} 25 \hspace{1cm} 30$

Val Glu Leu Asn Lys Arg Leu Gln Gln Thr Glu Arg Glu Asp Leu Leu 35 40 45

Glu Lys Lys Leu Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met Arg
50 55 60

Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg
65 70 75 80

Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile Asp
85 90 95

- Arg Leu Gln Gly Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu Leu 100 105 110
- Arg Ser Glu Leu Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser Arg 115 120 125
- Ser Met Asp Gln Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln Ser 130 135 140
- Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Ile Asn Ser Glu
 145 150 155 160
- Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg Lys 165 170 175
- Lys Ser Ser Cys Ser Leu Ser Val Ala Glu Val Asp Arg His Ile Glu 180 185 190
- Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr Val 195 200 205
- Glu Glu Ile Glu Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu Ala 210 215 220
- Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu Glu 225 230 235 240
- Asn Glu Ser Leu Thr Ala Met Leu Cys Ser Lys Glu Glu Glu Leu Asn 245 250 255
- Arg Thr Lys Ala Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg Leu 260 265 270
- Arg Arg Val Arg Glu Leu Gln Thr Arg Leu Gln Ser Val Gln Ala 275 280 285
- Thr Gly Pro Ser Ser Pro Gly Arg Leu Thr Ser Thr Asn Arg Pro Ile 290 295 300
- Asn Pro Ser Thr Gly Glu Leu Ser Thr Ser Ser Ser Ser Asn Asp Ile 305 310 315 320
- Pro Ile Ala Lys Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg Ser 325 330 335
- Glu Ser Ser Ser Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser Ser 340 345 350

- Ile Gly Val Ser Ser Ser Val Ala Glu His Leu Ala His Ser Leu Gln 355 360 365
- Asp Cys Ser Asn Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His Gly 370 375 380
- Ser Ala Ile Ser Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr Glu 385 390 395 400
- Arg Leu Asn Ser Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu Leu 405 410 415
- Thr Ile Thr Leu Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser Met 420 425 430
- Leu Val Gly Lys Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala Leu 435 440 445
- Gln Tyr Ser Glu Gln Cys Ile Glu Ala Tyr Glu Leu Leu Leu Ala Leu 450 455 460
- Ala Glu Ser Glu Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala Gly 465 470 475 480
- Val Gly Ser Ser Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr Gln
 485 490 495
- Met Leu Lys Arg Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala Ala 500 505 510
- Lys Ala Leu Leu Met Lys Leu Asp Gly Ser Cys Gly Gly Ala Phe Ala 515 520 525
- Val Ala Gly Cys Ser Val Gln Pro Trp Glu Ser Leu Ser Ser Asn Ser 530 540
- His Thr Ser Thr Thr Ser Ser Thr Ala Ser Ser Cys Asp Thr Glu Phe 545 550 555 560
- Thr Lys Glu Asp Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu Lys 565 570 575
- Asn Asp Arg Ala Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile 580 585 590
- His Ile Asp Pro Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser Gln 595 600 605

- Arg Leu Asp Leu Glu Asn Ala Val Leu Met Gln Glu Leu Met Ala Met 610 620
- Lys Glu Glu Met Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu Lys 625 630 635 640
- Glu Lys Lys Ala Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu 645 650 655
- Gln Ala Tyr Leu Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu 660 665 670
- Gln Lys Glu Gln Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly Ser 675 680 685
- Lys Asp Lys Pro Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu 690 695 700
- Ser Leu Ala Glu Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala Ala 705 710 715 720
- Glu Phe Thr Asn Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg Val
 725 730 735
- Gln Glu Leu Val Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu Ile 740 745 750
- Arg His Gln Gln Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala Asn 755 760 765
- Ser Asn Leu Val Ala Ala Tyr Glu Lys Ala Lys Lys Lys His Gln Asn
 770 780
- Lys Leu Lys Lys Leu Glu Ser Gln Met Met Ala Met Val Glu Arg His 785 790 795 800
- Glu Thr Gln Val Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu Glu 805 810 815
- Glu Asn Ser Arg Pro His Thr Asn Glu Thr Ser Leu 820 825

<210> 27

<211> 672

<212> PRT

<213> human

<	4	0	0	>	2	7
---	---	---	---	---	---	---

- Met Ala Asp Val Phe Pro Gly Asn Asp Ser Thr Ala Ser Gln Asp Val

 1 5 10 15
- Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His
- Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr
 35 40 45
- Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gly Gly 50 55 60
- Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu
 65 70 75 80
- Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp
 85 90 95
- Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro 100 105 110
- Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln
 115 120 125
- Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Lys Gln Cys Val 130 135 140
- Ile Asn Val Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly
 145 150 155 160
- Arg Ile Tyr Leu Lys Ala Glu Val Ala Asp Glu Lys Leu His Val Thr 165 170 175
- Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser 180 185 190
- Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser 195 200 205
- Lys Gln Lys Thr Lys Thr Ile Arg Ser Thr Leu Asn Pro Gln Trp Asn 210 215 220
- Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu 225 230 235 240
- Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met

245 250 255

Gly	Ser	Leu	Ser	Phe	Gly	Val	Ser	Glu	Leu	Met	Lys	Met	Pro	Ala	Ser
			260					265					270		

- Gly Trp Tyr Lys Leu Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val 275 280 285
- Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys 290 295 300
- Phe Glu Lys Ala Lys Leu Gly Pro Ala Gly Asn Lys Val Ile Ser Pro 305 310 315 320
- Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu 325 330 335
- Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys 340 345 350
- Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys 355 360 365
- Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr 370 375 380
- Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu 385 390 395 400
- Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val 405 410 415
- Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val 420 425 430
- Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser 435 440 445
- Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu 450 455 460
- Lys Leu Asp Asn Val Met Leu Asp Ser Glu Gly His Ile Lys Ile Ala 465 470 475 480
- Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg
 485 490 495
- Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr

500 505 510

Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu 515 520 525

Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp 530 535 540

Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser 545 550 555 560

Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys His
565 570 575

Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg 580 585 590

Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg 595 600 605

Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu 610 615 620

Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro 625 630 635 640

Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe 645 650 655

Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val 660 665 670

<210> 28

<211> 471

<212> PRT

<213> human

<400> 28

Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn

1 10 15

Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe 20 25 30

- Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp 35 40 45
- Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser 50 55 60
- Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu 65 70 75 80
- Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile 85 90 95
- Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe 100 105 110
- Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met 115 120 125
- Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro 130 135 140
- Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr 145 150 155 160
- Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala 165 170 175
- Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala 180 185 190
- Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met 195 200 205
- Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu 210 215 220
- Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe 225 230 235 240
- Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu 245 250 255
- Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu 260 265 270
- Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser 275 280 285

Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly 290 295 300

Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys 305 310 315

Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp 325 330 335

Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser 340 345 350

Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile 355 360 365

Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn 370 375 380

Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys 385 390 395 400

Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala 405 410 415

Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser 420 425 430

Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu 435 440 445

Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val 450 455 460

Asn Glu Lys Val Ser Cys Val 465 470

<210> 29

<211> 481

<212> PRT

<213> human

<400> 29

Met Ala Leu Ser Tyr Arg Val Ser Glu Leu Gln Ser Thr Ile Pro Glu
1 5 10 15

His Ile Leu Gln Ser Thr Phe Val His Val Ile Ser Ser Asn Trp Ser 20 25 30

- Gly Leu Gln Thr Glu Ser Ile Pro Glu Glu Met Lys Gln Ile Val Glu 35 40 45
- Glu Gln Gly Asn Lys Leu His Trp Ala Ala Leu Leu Ile Leu Met Val 50 55 60
- Ile Ile Pro Thr Ile Gly Gly Asn Thr Leu Val Ile Leu Ala Val Ser
 65 70 75 80
- Leu Glu Lys Lys Leu Gln Tyr Ala Thr Asn Tyr Phe Leu Met Ser Leu 85 90 95
- Ala Val Ala Asp Leu Leu Val Gly Leu Phe Val Met Pro Ile Ala Leu 100 105 110
- Leu Thr Ile Met Phe Glu Ala Met Trp Pro Leu Pro Leu Val Leu Cys
 115 120 125
- Pro Ala Trp Leu Phe Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met 130 135 140
- His Leu Cys Ala Ile Ser Val Asp Arg Tyr Ile Ala Ile Lys Lys Pro 145 150 155 160
- Ile Gln Ala Asn Gln Tyr Asn Ser Arg Ala Thr Ala Phe Ile Lys Ile 165 170 175
- Thr Val Val Trp Leu Ile Ser Ile Gly Ile Ala Ile Pro Val Pro Ile 180 185 190
- Lys Gly Ile Glu Thr Asp Val Asp Asn Pro Asn Asn Ile Thr Cys Val 195 200 205
- Leu Thr Lys Glu Arg Phe Gly Asp Phe Met Leu Phe Gly Ser Leu Ala 210 215 220
- Ala Phe Phe Thr Pro Leu Ala Ile Met Ile Val Thr Tyr Phe Leu Thr 225 230 235 240
- Ile His Ala Leu Gln Lys Lys Ala Tyr Leu Val Lys Asn Lys Pro Pro
 245 250 255
- Gln Arg Leu Thr Trp Leu Thr Val Ser Thr Val Phe Gln Arg Asp Glu 260 265 270
- Thr Pro Cys Ser Ser Pro Glu Lys Val Ala Met Leu Asp Gly Ser Arg 275 280 285

Lys Asp Lys Ala Leu Pro Asn Ser Gly Asp Glu Thr Leu Met Arg Arg 290 295 300

Thr Ser Thr Ile Gly Lys Lys Ser Val Gln Thr Ile Ser Asn Glu Gln 305 310 315 320

Arg Ala Ser Lys Val Leu Gly Ile Val Phe Phe Leu Phe Leu Met 325 330 335

Trp Cys Pro Phe Phe Ile Thr Asn Ile Thr Leu Val Leu Cys Asp Ser 340 345 350

Cys Asn Gln Thr Thr Leu Gln Met Leu Leu Glu Ile Phe Val Trp Ile 355 360 365

Gly Tyr Val Ser Ser Gly Val Asn Pro Leu Val Tyr Thr Leu Phe Asn 370 375 380

Lys Thr Phe Arg Asp Ala Phe Gly Arg Tyr Ile Thr Cys Asn Tyr Arg 385 390 395 400

Ala Thr Lys Ser Val Lys Thr Leu Arg Lys Arg Ser Ser Lys Ile Tyr
405 410 415

Phe Arg Asn Pro Met Ala Glu Asn Ser Lys Phe Phe Lys Lys His Gly 420 425 430

Ile Arg Asn Gly Ile Asn Pro Ala Met Tyr Gln Ser Pro Met Arg Leu 435 440 445

Arg Ser Ser Thr Ile Gln Ser Ser Ser Ile Ile Leu Leu Asp Thr Leu 450 455 460

Leu Leu Thr Glu Asn Glu Gly Asp Lys Thr Glu Glu Gln Val Ser Tyr 465 470 475 480

Val

<210> 30

<211> 2843

<212> PRT

<213> human

<400> 30

Met Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu

10 15	1 5	10	15
-------	-----	----	----

Lys	Met	Glu	Asn	Ser	Asn	Leu	Arg	Gln	Glu	Leu	Glu	Asp	Asn	Ser	Asn
			20					25					3.0		

- His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu 35 40 45
- Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
 50 55 60
- Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser 65 70 75 80
- Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr 85 90 95
- Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro 100 105 110
- Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg 115 120 125
- Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu 130 135 140
- Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu 165 170 175
- Asn Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu 180 185 190
- Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
 195 200 205
- Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile 210 215 220
- Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr 225 230 235 240
- Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp 245 250 255
- Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala

260 265 270

Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr
275 280 285

Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu 290 295 300

Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser 305 310 315 320

Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala 325 330 335

Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys 340 345 350

Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val 355 360 365

Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser 370 375 380

Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly 385 390 395 400

Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr 405 410 415

Cys Ser Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp 420 425 430

Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro 435 440 445

Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His 450 455 460

Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln 465 470 475 480

Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr 485 490 495

Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp 500 505 510

Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala

515 520 525

Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile 530 535 540

Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys 545 550 555 560

Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala 565 570 575

Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu 580 585 590

Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala 595 600 605

Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser 610 615 620

Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg 625 630 635 640

Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu 645 650 655

Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His
660 665 670

Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser 675 680 685

Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val 690 695 700

Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met 705 710 715 720

Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys
725 730 735

Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu
740 745 750

His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His
755 760 765

Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Ile Ser Pro Lys Ala Ser

770 775 780

His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val
785 790 795 800

Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr 805 810 815

Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro 820 825 830

Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys 835 840 845

Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His 850 855 860

Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile 865 870 875 880

Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala 885 890 895

Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu 900 905 910

His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala 915 920 925

His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn 930 935 940

Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser 945 950 955 960

Asn Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg 965 970 975

Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser 980 985 990

Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile 995 1000 1005

His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro 1010 1015 1020

Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg

a M

- Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser 1060 1065 1070

 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Agn Agn Lyg Lig Low Lyg
- Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys 1075 1080 1085

Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile

- Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser 1090 1095 1100
- Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly 1105 1110 1115 1120
- Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu 1125 1130 1135
- Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln 1140 1145 1150
- His Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu 1155 1160 1165
- Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Ile Leu Lys Ala 1170 1175 1180
- Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser 1185 1190 1195 1200
- Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu
 1205 1210 1215
- Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His 1220 1225 1230
- Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr 1235 1240 1245
- Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val 1250 1255 1260
- Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu 1265 1270 1275 1280
- Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala

- Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly 1300 1305 1310
- Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln 1315 1320 1325
- His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser 1330 1335 1340
- Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser 1345 1350 1355 1360
- Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr 1365 1370 1375
- Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser 1380 1385 1390
- Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu 1395 1400 1405
- Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro 1410 1415 1420
- Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro 1425 1430 1435 1440
- Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys 1445 1450 1455
- Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val 1460 1465 1470
- Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu 1475 1480 1485
- Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser 1490 1495 1500
- Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val 1505 1510 1515 1520
- Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu 1525 1530 1535
- Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu

- Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp 1555 1560 1565
- Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro 1570 1580
- Thr Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys 1585 1590 1595 1600
- Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys
 1605 1610 1615
- Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe 1620 1625 1630
- Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro 1635 1640 1645
- Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser 1650 1660
- Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln 1665 1670 1680
- Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser 1685 1690 1695
- Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu 1700 1705 1710
- Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile 1715 1720 1725
- Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys 1730 1740
- Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro 1745 1750 1755 1760
- Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val 1765 1770 1775
- Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn 1780 1785 1790
- Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn

1795 1800 1805

Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn 1810 1815 1820

Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe 1825 1830 1835 1840

Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe 1845 1850 1855

Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val 1860 1865 1870

Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys 1875 1880 1885

Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln 1890 1895 1900

Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg 1905 1910 1915 1920

Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser 1925 1930 1935

Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln 1940 1945 1950

Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser 1955 1960 1965

Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn 1970 1975 1980

Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser 1985 1990 1995 2000

Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp 2005 2010 2015

Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile 2020 2025 2030

Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro 2035 2040 2045

Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser

- Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu 2065 2070 2075 2080
- Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser 2085 2090 2095
- Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val 2100 2105 2110
- Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala 2115 2120 2125
- Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu 2130 2135 2140
- Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr 2145 2150 2155 2160
- Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu 2165 2170 2175
- Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys
 2180 2185 2190
- Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu 2195 2200 2205
- Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile 2210 2215 2220
- Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser 2225 2230 2235 2240
- Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
 2245 2250 2255
- Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg 2260 2265 2270
- Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln 2275 2280 2285
- Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser 2290 2295 2300
- Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro

The state of the s

Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile

Ser Pro Pro Asn Lys Ile Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser

Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser

Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu

Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly

Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu

Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser

Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro

Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser

Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln

Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His

Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser

Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala

- Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val 2580 2585 2590
- Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala 2595 2600 2605
- Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn 2610 2615 2620
- Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser 2625 2630 2635 2640
- Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp 2645 2650 2655
- Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670
- Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu 2675 2680 2685
- Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln 2690 2695 2700
- Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn 2705 2710 2715 2720
- Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr 2725 2730 2735
- Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn 2740 2745 2750
- Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser Ser 2755 2760 2765
- Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe 2770 2775 2780
- Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala 2785 2790 2795 2800
- Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg 2805 2810 2815
- Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys

```
The first first from the first first
```

```
Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
        2835
                            2840
 <210> 31
 <211> 65
 <212> DNA
 <213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
<220>
<221> misc_feature
<222> (9)..(17)
<223> N=A, T, C or G
<220>
<221> misc_feature
<222> (24)..(32)
<223> N=A, T, C, or G
<220>
<221> misc feature
<222> (39)..(41)
<223> N=A, T, C or G
<220>
<221> misc_feature
<222> (51)..(53)
<223> N=A, T, C or G
<400> 31
cggaattcnn nnnnnnnaac agcnnnnnnn nnaatgaann ncaaagtctg nnntgaggat 60
cctca
                                                                    65
<210> 32
<211> 65
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial
      Sequence:source:synthesized
```

```
<220>
<221> misc_feature
<222> (18)..(23)
<223> N= A, T ,C or G
<220>
<221> misc_feature
<222> (33)..(38)
<223> N=A, T, C or G
<220>
<221> misc_feature
<222> (42)..(50)
<223> N=A, T, C or G
<400> 32
cggaattcga ctcagaannn nnnaacttca gannnnnnat cnnnnnnnn gtctgaggat 60
cctca
                                                           65
<210> 33
<211> 65
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial
     Sequence:source:synthesized
<220>
<221> misc_feature
<222> (9)..(53)
<223> N=A, T, C or G
<400> 33
cctca
                                                           65
```